AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

Claims 1-14 (Canceled).

15. (Previously Presented) Method for determining the presence or absence of HBV genotype A in a biological sample, comprising:

(i) optionally releasing, isolating and/or concentrating the polynucleic acids present in the sample;

(ii) optionally amplifying the HBsAg region, or part thereof, of the HBV gene present in said sample with at least one suitable primer pair;

(iii) hybridizing the polynucleic acids of step (i) or (ii) with at least one nucleotide probe of about 5 to 50 nucleotides long hybridizing specifically to a HBV genotype A specific target sequence in the HBsAg region of HBV;

(iv) detecting the hybrid(s) formed in step (iii);

(v) inferring the HBV genotype present in said sample from the hybridization signal(s) obtained in step (iv).

16. (Previously Presented) Method according to claim 15, wherein the HBV genotype A specific target is selected from the group consisting of SEQ ID NOs: 279-313.

17. (Previously Presented) Method according to claim 15, wherein the HBV genotype A specific target sequence is selected from the group consisting of SEQ ID NO: 77, SEQ ID NO: 140 and SEQ ID NO: 193, or the complement thereof.

18. (Previously Presented) Method according to any one of claims 15-17, characterized further by determining the presence or absence of HBV genotype B, wherein the probe(s) of step (iii) hybridizes specifically to a HBV genotype B specific target sequence in the HBsAg region.

19. (Previously Presented) Method according to claim 18, wherein the HBV genotype B specific target sequence is SEQ ID NO: 78, or the complement thereof.

20. (Previously Presented) Method according to any one of claims 15-17, characterized further by determining the presence or absence of HBV genotype C, wherein the probe(s) of step (iii) hybridizes specifically to a HBV genotype C specific target sequence.

21. (Previously Presented) Method according to claims 20, wherein the HBV genotype C specific target sequence is selected from the group consisting of SEQ ID NO: 153, SEQ ID NO: 154 and SEQ ID NO: 204, or the complement thereof.

22. (Previously Presented) Method according to any one of claims 15-17, characterized further by determining the presence or absence of HBV genotype D,

wherein the probe(s) of step (iii) hybridizes specifically to a HBV genotype D specific target sequence.

23. (Previously Presented) Method according to claim 22, wherein the HBV genotype D specific target is selected from the group consisting of SEQ ID NO: 165 and SEQ ID NO: 208, or the complement thereof.

24. (Previously Presented) Method according to any one of claims 15-17, characterized further by determining the presence or absence of HBV genotype E, wherein the probe(s) of step (iii) hybridizes specifically to a HBV genotype E specific target sequence.

25. (Previously Presented) Method according to claim 24, wherein the HBV genotype E specific target sequence is selected from the group consisting of SEQ ID NO: 172 and SEQ ID NO: 213, or the complement thereof.

26. (Previously Presented) Method according to any one of claims 15-17, characterized further by determining the presence or absence of HBV genotype F, wherein the probe(s) of step (iii) hybridizes specifically to a HBV genotype F specific target sequence.

27. (Previously Presented) Method according to claim 26, wherein the HBV genotype F specific target sequence is selected from the group consisting of SEQ ID NO: 186, SEQ ID NO: 216 and SEQ ID NO: 219, or the complement thereof.

28. (Previously Presented) Method according to any one of claims 15-17 wherein the primer is selected from the group consisting of SEQ ID NOs: 75-76, 94, 105, 112 and 134-135.

29. (Previously Presented) Method according to any one of claims 15-17 wherein step (iii) is a reverse hybridization step.

30. (Previously Presented) Probe of about 5 to 50 nucleotides long suitable for hybridizing in a method as defined in any of one claims 15-17.

31. (Previously Presented) Probe of about 5 to 50 nucleotides long specifically hybridizing to a HBV genotype A specific target sequence in the HBsAg region of HBV, said target sequence being selected from the group consisting of SEQ ID NO: 77, SEQ ID NO: 140, SEQ ID NO: 148 and SEQ ID NO: 193, or the complement thereof.

32. (Previously Presented) A composition comprising at least two probes of about 5 to 50 nucleotides long specifically hybridizing to a HBV genotype specific target sequence in the HbsAg region of HBV, said target sequence for genotype A being selected from the group consisting of SEQ ID NO: 77, SEQ ID NO: 140, SEQ ID NO: 148 and SEQ ID NO: 193, or the complement thereof; for genotype B being selected from the group consisting of SEQ ID NO: 78 and SEQ ID NO: 148, or the complement thereof being; for genotype C being selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 153, SEQ ID NO: 154 and SEQ ID NO: 204, or the complement thereof; for genotype D being selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 165 and SEQ ID NO: 208, or the complement thereof; for genotype E

being selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 172, SEQ ID NO: 177 and SEQ ID NO: 213, or the complement thereof; for genotype F being selected from the group consisting of SEQ ID NO: 177, SEQ ID NO: 216, SEQ ID NO: 219 and SEQ ID NO: 186, or the complement thereof.

Claim 33. (Canceled)

34. (Previously Presented) Assay kit for diagnosing or monitoring HBV genotypes present in a biological sample comprising at least one of the probes according to claim 30, possibly fixed to a solid support.